1642

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/192,861A*

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TIME: 11:46:52

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This Raw Listing contains the General
Information Section and up to the first 5 pages.

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 1                         SEQUENCE LISTING
 2
 3   (1)    General Information:                        ENTERED
 4
 5        (i) APPLICANT: Le, Junming
 6                       Vilcek, Jan
 7                       Daddona, Peter E.
 8                       Ghrayeb, John
 9                       Knight, David M.
10                       Siegel, Scott A.
11
12     (ii) TITLE OF INVENTION: METHODS OF TREATING TNFÁ-MEDIATED DISEASE USING
13          CHIMERIC ANTI-TNF ANTIBODIES (As Amended)
14
15    (iii) NUMBER OF SEQUENCES: 19
16
17     (iv) CORRESPONDENCE ADDRESS:
18          (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
19          (B) STREET: Two Militia Drive
20          (C) CITY:  Lexington
21          (D) STATE: Massachusetts
22          (E) COUNTRY: USA
23          (F) ZIP: 02173
24
25      (v) COMPUTER READABLE FORM:
26          (A) MEDIUM TYPE: Floppy disk
27          (B) COMPUTER: IBM PC compatible
28          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29          (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
30
31     (vi) CURRENT APPLICATION DATA:
32          (A) APPLICATION NUMBER: 08/192,861
33          (B) FILING DATE: 04-FEB-1994
34
35    (vii) PRIOR APPLICATION DATA:
36          (A) APPLICATION NUMBER: US 08/013,413
37          (B) FILING DATE: 02-FEB-1993
38
39    (vii) PRIOR APPLICATION DATA:
40          (A) APPLICATION NUMBER: US 08/010,406
41          (B) FILING DATE: 29-JAN-1993
42
43    (vii) PRIOR APPLICATION DATA:
44          (A) APPLICATION NUMBER: US 07/943,852
45          (B) FILING DATE: 11-SEP-1992
46
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47        (vii) PRIOR APPLICATION DATA:
48              (A) APPLICATION NUMBER: US 07/853,606
49              (B) FILING DATE: 18-MAR-1992
50
51        (vii) PRIOR APPLICATION DATA:
52              (A) APPLICATION NUMBER: US 07/670,827
53              (B) FILING DATE: 18-MAR-1991
54
55      (viii) ATTORNEY/AGENT INFORMATION:
56              (A) NAME: Brook, David E.
57              (B) REGISTRATION NUMBER: 22,592
58              (C) REFERENCE/DOCKET NUMBER: NYU93-01M2
59
60        (ix) TELECOMMUNICATION INFORMATION:
61              (A) TELEPHONE: (781) 861-6240
62              (B) TELEFAX: (781) 861-9540
63
64
65    (2) INFORMATION FOR SEQ ID NO:1:
66
67        (i) SEQUENCE CHARACTERISTICS:
68              (A) LENGTH: 157 amino acids
69              (B) TYPE: amino acid
70              (D) TOPOLOGY: linear
71
72       (ii) MOLECULE TYPE: peptide
73
74       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
75
76      Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
77      1               5                   10                  15
78
79      Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
80                      20                  25                  30
81
82      Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
83              35                  40                  45
84
85      Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
86          50                  55                  60
87
88      Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
89      65                  70                  75                  80
90
91      Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
92                          85                  90                  95
93
94      Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
95                  100                 105                 110
96
97      Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
98              115                 120                 125
99
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100        Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
101            130                 135                 140
102
103        Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
104            145                 150                 155
105
106
107    (2) INFORMATION FOR SEQ ID NO:2:
108
109        (i) SEQUENCE CHARACTERISTICS:
110            (A) LENGTH: 321 base pairs
111            (B) TYPE: nucleic acid
112            (C) STRANDEDNESS: single
113            (D) TOPOLOGY: linear
114
115
116    (ii) MOLECULE TYPE: cDNA
117
118
119    (ix) FEATURE:
120            (A) NAME/KEY: CDS
121            (B) LOCATION: 1..321
122
123
124
125
126    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
127
128    GAC ATC TTG CTG ACT CAG TCT CCA GCC ATC CTG TCT GTG AGT CCA GGA   48
129    Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
130     1               5                  10                  15
131
132    GAA AGA GTC AGT TTC TCC TGC AGG GCC AGT CAG TTC GTT GGC TCA AGC   96
133    Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
134                20                  25                  30
135
136    ATC CAC TGG TAT CAG CAA AGA ACA AAT GGT TCT CCA AGG CTT CTC ATA  144
137    Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
138                35                  40                  45
139
140    AAG TAT GCT TCT GAG TCT ATG TCT GGG ATC CCT TCC AGG TTT AGT GGC  192
141    Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
142                50                  55                  60
143
144    AGT GGA TCA GGG ACA GAT TTT ACT CTT AGC ATC AAC ACT GTG GAG TCT  240
145    Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
146     65                  70                  75                  80
147
148    GAA GAT ATT GCA GAT TAT TAC TGT CAA CAA AGT CAT AGC TGG CCA TTC  288
149    Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
150                85                  90                  95
151
152    ACG TTC GGC TCG GGG ACA AAT TTG GAA GTA AAA                       321
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153   Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
154               100                 105
155
156
157   (2) INFORMATION FOR SEQ ID NO:3:
158
159       (i) SEQUENCE CHARACTERISTICS:
160           (A) LENGTH: 107 amino acids
161           (B) TYPE: amino acid
162           (D) TOPOLOGY: linear
163
164       (ii) MOLECULE TYPE: protein
165
166       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
167
168   Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
169    1               5                 10                  15
170
171   Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
172               20                  25                  30
173
174   Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
175           35                  40                  45
176
177   Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
178       50                  55                  60
179
180   Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
181    65                  70                  75                  80
182
183   Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
184               85                  90                  95
185
186   Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
187               100                 105
188
189   (2) INFORMATION FOR SEQ ID NO:4:
190
191       (i) SEQUENCE CHARACTERISTICS:
192           (A) LENGTH: 357 base pairs
193           (B) TYPE: nucleic acid
194           (C) STRANDEDNESS: single
195           (D) TOPOLOGY: linear
196
197       (ii) MOLECULE TYPE: cDNA
198
199
200       (ix) FEATURE:
201           (A) NAME/KEY: CDS
202           (B) LOCATION: 1..357
203
204
205       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
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206
207    GAA GTG AAG CTT GAG GAG TCT GGA GGA GGC TTG GTG CAA CCT GGA GGA    48
208    Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
209     1               5                  10                  15
210
211    TCC ATG AAA CTC TCC TGT GTT GCC TCT GGA TTC ATT TTC AGT AAC CAC    96
212    Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
213                 20                  25                  30
214
215    TGG ATG AAC TGG GTC CGC CAG TCT CCA GAG AAG GGG CTT GAG TGG GTT    144
216    Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
217                 35                  40                  45
218
219    GCT GAA ATT AGA TCA AAA TCT ATT AAT TCT GCA ACA CAT TAT GCG GAG    192
220    Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
221         50                  55                  60
222
223    TCT GTG AAA GGG AGG TTC ACC ATC TCA AGA GAT GAT TCC AAA AGT GCT    240
224    Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
225     65                  70                  75                  80
226
227    GTC TAC CTG CAA ATG ACC GAC TTA AGA ACT GAA GAC ACT GGC GTT TAT    288
228    Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
229                     85                  90                  95
230
231    TAC TGT TCC AGG AAT TAC TAC GGT AGT ACC TAC GAC TAC TGG GGC CAA    336
232    Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
233                 100                 105                 110
234
235    GGC ACC ACT CTC ACA GTC TCC                                       357
236    Gly Thr Thr Leu Thr Val Ser
237                 115
238
239
240    (2) INFORMATION FOR SEQ ID NO:5:
241
242        (i) SEQUENCE CHARACTERISTICS:
243            (A) LENGTH: 119 amino acids
244            (B) TYPE: amino acid
245            (D) TOPOLOGY: linear
246
247        (ii) MOLECULE TYPE: protein
248
249
250
251        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
252
253    Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
254     1               5                  10                  15
255
256    Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
257                 20                  25                  30
258
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/192,861A*

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